

10/767.701

1A 4/10/06

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 2, 2006, 05:07:14 ; Search time 229 Seconds

(without alignments)
677.800 Million cell updates/sec

Title: US-10-767-701-44293

Perfect score: 1131

Sequence: 1 MGQSLIVAFVARGVTILAE.....IIIALILITLSCVCHGPKCH 220

Scoring table: BLOSUM62

Gapop 10.0 , Gapext: 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database: UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------|
| 1 | 1100 | 97.3 | 220 | 2 | Q69WS1_ORYSA |
| 2 | 1091 | 96.5 | 220 | 2 | Q84S21_ORYSA |
| 3 | 1016 | 88.8 | 285 | 1 | VA725_ARATH |
| 4 | 1010 | 88.3 | 219 | 1 | VA721_ARATH |
| 5 | 1010 | 88.3 | 219 | 2 | Q681L9_ARATH |
| 6 | 1006 | 88.9 | 219 | 2 | Q681H0_ARATH |
| 7 | 1003 | 88.7 | 220 | 1 | VA726_ARATH |
| 8 | 995 | 88.0 | 221 | 1 | VA722_ARATH |
| 9 | 933 | 82.5 | 194 | 2 | Q7X9C5_PIRHY |
| 10 | 848.5 | 75.0 | 222 | 2 | VA724_ARATH |
| 11 | 848.5 | 75.0 | 222 | 2 | Q6ID96_ARATH |
| 12 | 795 | 70.3 | 215 | 2 | Q5URW2_HORVD |
| 13 | 792 | 70.0 | 217 | 1 | VA723_ARATH |
| 14 | 786 | 69.5 | 218 | 2 | Q6RUK3_TRIMO |
| 15 | 779 | 68.9 | 181 | 2 | Q67YV9_ARATH |
| 16 | 741.5 | 65.6 | 248 | 2 | Q8H3D2_ORYSA |
| 17 | 732.5 | 64.8 | 240 | 1 | VA727_ARATH |
| 18 | 732.5 | 64.8 | 240 | 2 | Q53XB0_ARATH |
| 19 | 715 | 63.2 | 241 | 2 | Q6YZ18_ORYSA |
| 20 | 413.5 | 36.6 | 219 | 1 | VA713_ARATH |
| 21 | 407 | 36.0 | 221 | 1 | VA714_ARATH |
| 22 | 396 | 35.0 | 221 | 1 | VA713_ARATH |
| 23 | 394.5 | 34.9 | 260 | 2 | Q86A07_DICDI |
| 24 | 387 | 34.2 | 220 | 2 | Q6DDH7_XENTIA |
| 25 | 384 | 34.0 | 220 | 2 | Q5EL74_CHICK |
| 26 | 383 | 33.9 | 220 | 2 | P70280_MOUSE |
| 27 | 380 | 33.6 | 219 | 1 | SYBL1_HUMAN |
| 28 | 380 | 33.6 | 220 | 2 | Q53GY7_HUMAN |
| 29 | 379 | 33.5 | 87 | 2 | Q4U3F2_IPOBA |
| 30 | 377.5 | 33.4 | 219 | 1 | VA712_ARATH |
| 31 | 377 | 33.3 | 219 | 1 | SYBL1_PONPY |

| | | | | | |
|-----|-------|------|-----|---|--------------|
| 32 | 377 | 33.3 | 220 | 2 | Q9JHWS_RAT |
| 33 | 372 | 32.9 | 221 | 2 | Q9LWKL_ORYSA |
| 34 | 360 | 31.8 | 223 | 2 | Q8S670_ORYSA |
| 35 | 346.5 | 30.6 | 226 | 2 | Q69S01_ORYSA |
| 36 | 343.5 | 30.4 | 218 | 2 | Q9V5C3_DROME |
| 37 | 338.5 | 29.9 | 218 | 2 | Q720P6_PARTH |
| 38 | 338.5 | 29.9 | 306 | 2 | Q560P1_CRYNE |
| 39 | 338.5 | 29.9 | 306 | 2 | Q5KXN6_CRYNE |
| 40 | 338 | 29.9 | 208 | 2 | Q81ET3_PLAF7 |
| 41 | 332 | 29.4 | 208 | 2 | Q4YCD2_PLABE |
| 42 | 327 | 28.9 | 216 | 2 | Q5ANW7_DICDI |
| 43 | 321 | 28.4 | 218 | 2 | Q70BD7_ANOGA |
| 44 | 302.5 | 26.7 | 242 | 2 | Q7S9T6_NEUCR |
| 45 | 299 | 26.4 | 236 | 2 | Q41187_GI2ZE |
| 46 | 298 | 26.3 | 173 | 2 | Q4T515_TETNG |
| 47 | 290.5 | 25.7 | 209 | 2 | Q4PHX9_USUMA |
| 48 | 277.5 | 24.5 | 179 | 2 | Q72409_HUMAN |
| 49 | 271.5 | 24.0 | 253 | 2 | Q4WM41_ASPEU |
| 50 | 259.5 | 22.9 | 263 | 2 | Q5AFV9_EMENT |
| 51 | 258 | 22.8 | 210 | 2 | Q720P5_PARTH |
| 52 | 255 | 22.5 | 210 | 2 | Q72113_PARTH |
| 53 | 254 | 22.5 | 230 | 2 | Q52FF5_MAGGR |
| 54 | 254 | 22.5 | 226 | 2 | Q6CFT6_YARLI |
| 55 | 252 | 22.3 | 155 | 2 | Q7YX68_CRYPV |
| 56 | 247 | 21.8 | 164 | 2 | Q4X063_PLACH |
| 57 | 245 | 21.7 | 206 | 2 | Q91RX2_ARATH |
| 58 | 244 | 21.6 | 181 | 2 | Q72U11_BRARE |
| 59 | 242 | 21.6 | 223 | 2 | Q8NKK9_ASPEU |
| 60 | 237 | 21.0 | 260 | 2 | Q584A7_HUMAN |
| 61 | 237 | 21.0 | 75 | 2 | Q5MDW3_TOBAN |
| 62 | 217.5 | 19.3 | 221 | 2 | Q7YUS4_9TRYF |
| 63 | 215 | 19.2 | 216 | 2 | Q5TUB0_9TRYF |
| 64 | 214 | 18.9 | 220 | 2 | Q4FY81_LEIMA |
| 65 | 201.5 | 17.8 | 115 | 2 | Q6CHZ4_YARLI |
| 66 | 200.5 | 17.7 | 121 | 1 | SYBL1_SCHPO |
| 67 | 199 | 17.6 | 215 | 2 | Q4QIG6_LEIMA |
| 68 | 198.5 | 17.6 | 135 | 2 | Q6BSW9_DBRHA |
| 69 | 197.5 | 17.5 | 112 | 2 | Q6C714_YARLI |
| 70 | 195.5 | 17.3 | 257 | 2 | Q4QC67_LEIMA |
| 71 | 194.5 | 17.2 | 118 | 2 | Q412M1_GI2ZE |
| 72 | 192.5 | 17.0 | 228 | 2 | Q513U3_ENTHI |
| 73 | 186 | 16.4 | 140 | 2 | Q610B0_BRARE |
| 74 | 185 | 16.4 | 117 | 1 | SNCL1_YEAST |
| 75 | 185 | 16.4 | 192 | 2 | Q6EFX0_ENTHI |
| 76 | 185 | 16.4 | 223 | 2 | Q26586_SCHMA |
| 77 | 184.5 | 16.3 | 109 | 2 | Q759C2_ASHGO |
| 78 | 182 | 16.1 | 245 | 2 | Q95XH1_CABEL |
| 79 | 181.5 | 16.0 | 84 | 2 | QAS246_TETNG |
| 80 | 181.5 | 16.0 | 124 | 2 | Q7SF83_NEUCR |
| 81 | 180 | 15.9 | 113 | 2 | Q6FT06_CANGA |
| 82 | 180 | 15.9 | 245 | 2 | Q61HR8_CABER |
| 83 | 178.5 | 15.8 | 111 | 2 | Q6B781_TRIRE |
| 84 | 178.5 | 15.8 | 120 | 2 | Q5SLN4_CRYNE |
| 85 | 178.5 | 15.8 | 120 | 2 | Q5KD71_CRYNE |
| 86 | 177.5 | 15.7 | 129 | 2 | Q6X173_DROYA |
| 87 | 177.5 | 15.7 | 132 | 2 | Q9V516_DROME |
| 88 | 177.5 | 15.7 | 129 | 2 | Q6RXX1_DROME |
| 89 | 177 | 15.6 | 127 | 2 | Q7P1S4_ANOGA |
| 90 | 176 | 15.6 | 119 | 2 | Q7RH0T_PLAYO |
| 91 | 176 | 15.6 | 127 | 2 | Q7PNS9_ANOGA |
| 92 | 176 | 15.6 | 127 | 2 | Q6ZC99_ORYSA |
| 93 | 175 | 15.5 | 108 | 2 | Q6OWU2_CABER |
| 94 | 175 | 15.5 | 109 | 2 | Q02495_CABEL |
| 95 | 174.5 | 15.4 | 115 | 1 | SNCL2_YEAST |
| 96 | 174.5 | 15.4 | 201 | 2 | Q9TYX9_CABEL |
| 97 | 174.5 | 15.4 | 231 | 2 | Q6C1D6_KIULA |
| 98 | 174 | 15.4 | 95 | 2 | Q6TMJ9_DICDI |
| 99 | 173 | 15.3 | 180 | 1 | STB_APLCA |
| 100 | 172.5 | 15.3 | 230 | 2 | Q7Z0T4_ENTHI |
| 101 | 172.5 | 15.3 | 230 | 2 | Q51CN2_ENTHI |
| 102 | 172 | 15.2 | 110 | 2 | Q6CY19_KIULA |
| 103 | 172 | 15.2 | 111 | 2 | Q7PT71_ANOGA |
| 104 | 172 | 15.2 | 145 | 2 | Q869G4_LYMST |

| | |
|--------|--------------|
| Q9JHWS | rattus norv |
| Q9LWKL | oryza sativ |
| Q8S670 | oryza sativ |
| Q69S01 | oryza sativ |
| Q9V5C3 | drosophila |
| Q720P6 | parametium |
| Q560P1 | cryptococcu |
| Q5KXN6 | cryptococcu |
| Q81ET3 | plasmodium |
| Q4YCD2 | plasmodium |
| Q5ANW7 | dicystoceti |
| Q70BD7 | anopheles g |
| Q7S9T6 | neutrospora |
| Q41187 | gibberella |
| Q4T515 | tetragodon n |
| Q4PHX9 | usiliago ma |
| Q72409 | homo sapien |
| Q4WM41 | aspergillus |
| Q5AFV9 | aspergillus |
| Q720P5 | parametium |
| Q72113 | parametium |
| Q52FF5 | magnaporthe |
| Q6CFT6 | yarrowia li |
| Q7YX68 | cryptospori |
| Q4X063 | plasmodium |
| Q91RX2 | arabidopsis |
| Q72U11 | brachydanto |
| Q8NKK9 | aspergillus |
| Q584A7 | homo sapien |
| Q5MDW3 | nicotiana t |
| Q7YUS4 | trypanosoma |
| Q5TUB0 | trypanosoma |
| Q4FY81 | leishmania |
| Q6CHZ4 | yarrowia li |
| Q92356 | schizosacch |
| Q4QIG6 | leishmania |
| Q6BSW9 | debaromyce |
| Q6C714 | yarrowia li |
| Q4QC67 | leishmania |
| Q412M1 | gibberella |
| Q513U3 | entamoeba h |
| Q610B0 | brachydanto |
| Q51Q30 | brachydanto |
| P31109 | saccharomyce |
| Q86FX0 | entamoeba h |
| Q26586 | schistosoma |
| Q759C2 | asbyia gose |
| Q95XH1 | caenorhabdi |
| QAS246 | tetradodon n |
| Q7SF83 | neutrospora |
| Q6FT06 | candida gla |
| Q61HR8 | caenorhabdi |
| Q6B781 | trichoderma |
| Q5SLN4 | cryptococcu |
| Q5KD71 | cryptococcu |
| Q6X173 | drosophila |
| Q9V516 | drosophila |
| Q6RXX1 | drosophila |
| Q7P1S4 | anopheles g |
| Q7RH0T | plasmodium |
| Q7PNS9 | anopheles g |
| Q6ZC99 | oryza sativ |
| Q6OWU2 | caenorhabdi |
| Q02495 | caenorhabdi |
| P31328 | saccharomyce |
| Q9TXK9 | caenorhabdi |
| Q6C1D6 | kluyveromyce |
| Q6TMJ9 | dictyococci |
| Q6EMJ9 | dictyococci |
| P35589 | epilysia cal |
| Q7Z0T4 | entamoeba h |
| Q51CN2 | entamoeba h |
| Q6CY19 | kluyveromyce |
| Q7PT71 | anopheles g |
| Q869G4 | lymanaea sca |

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OM: protein search, using sw model

Run on: March 2, 2006, 05:07:39 / Search time 186 Seconds

(without alignments)
519.695 Million cell updates/sec

Title: US-10-767-701-44293

Perfect score: 1131

Sequence: 1 MGQOSLIYAFVARGVTLAE.....IIIALIIILISVCHFKCH 220

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database: A_Geneseq_21.*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003s:*
7: geneseqp2004s:*
8: geneseqp2005s:*
9: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 1131 | 100.0 | 244 | 8 | ADY04217 Plant ful |
| 2 | 1131 | 100.0 | 244 | 8 | ADY04217 Plant ful |
| 3 | 1131 | 100.0 | 244 | 8 | ADY04217 Plant ful |
| 4 | 1131 | 100.0 | 244 | 8 | ADY04217 Plant ful |
| 5 | 1131 | 100.0 | 244 | 8 | ADY04217 Plant ful |
| 6 | 1131 | 100.0 | 244 | 8 | ADY04217 Plant ful |
| 7 | 1131 | 100.0 | 244 | 8 | ADY04217 Plant ful |
| 8 | 1131 | 100.0 | 244 | 8 | ADY04217 Plant ful |
| 9 | 1131 | 100.0 | 244 | 8 | ADY04217 Plant ful |
| 10 | 1131 | 100.0 | 244 | 8 | ADY04217 Plant ful |
| 11 | 1131 | 100.0 | 244 | 8 | ADY04217 Plant ful |
| 12 | 1131 | 100.0 | 244 | 8 | ADY04217 Plant ful |
| 13 | 1131 | 100.0 | 244 | 8 | ADY04217 Plant ful |
| 14 | 1131 | 100.0 | 244 | 8 | ADY04217 Plant ful |
| 15 | 1131 | 100.0 | 244 | 8 | ADY04217 Plant ful |
| 16 | 1131 | 100.0 | 244 | 8 | ADY04217 Plant ful |
| 17 | 1131 | 100.0 | 244 | 8 | ADY04217 Plant ful |
| 18 | 1131 | 100.0 | 244 | 8 | ADY04217 Plant ful |
| 19 | 1131 | 100.0 | 244 | 8 | ADY04217 Plant ful |
| 20 | 1131 | 100.0 | 244 | 8 | ADY04217 Plant ful |
| 21 | 1131 | 100.0 | 244 | 8 | ADY04217 Plant ful |
| 22 | 1131 | 100.0 | 244 | 8 | ADY04217 Plant ful |
| 23 | 1131 | 100.0 | 244 | 8 | ADY04217 Plant ful |
| 24 | 1131 | 100.0 | 244 | 8 | ADY04217 Plant ful |

| | | | | | |
|----|-------|------|-----|---|--------------------|
| 25 | 784 | 69.3 | 232 | 8 | ADY67636 Plant ful |
| 26 | 744 | 65.8 | 155 | 3 | AAB32593 Arabidops |
| 27 | 740 | 65.4 | 161 | 3 | AAB32883 Arabidops |
| 28 | 732.5 | 64.8 | 240 | 3 | AAG54006 Arabidops |
| 29 | 732.5 | 64.8 | 240 | 3 | AAG54005 Arabidops |
| 30 | 732.5 | 64.8 | 240 | 3 | AAG54005 Arabidops |
| 31 | 732.5 | 64.8 | 240 | 3 | AAG54005 Arabidops |
| 32 | 732.5 | 64.8 | 240 | 3 | AAG54005 Arabidops |
| 33 | 732.5 | 64.8 | 240 | 3 | AAG54005 Arabidops |
| 34 | 732.5 | 64.8 | 240 | 3 | AAG54005 Arabidops |
| 35 | 732.5 | 64.8 | 240 | 3 | AAG54005 Arabidops |
| 36 | 718 | 63.5 | 166 | 3 | AAG30423 Arabidops |
| 37 | 718 | 63.5 | 166 | 3 | AAG30423 Arabidops |
| 38 | 714 | 63.1 | 257 | 8 | ADY06189 Arabidops |
| 39 | 712 | 63.0 | 247 | 8 | ADY22656 Arabidops |
| 40 | 712 | 63.0 | 247 | 8 | ADY22656 Arabidops |
| 41 | 711 | 62.9 | 155 | 3 | AAG37515 Arabidops |
| 42 | 699 | 61.5 | 139 | 3 | AAG44785 Arabidops |
| 43 | 695 | 61.5 | 150 | 3 | AAB32605 Arabidops |
| 44 | 650 | 57.5 | 141 | 3 | AAG37012 Arabidops |
| 45 | 650 | 57.5 | 141 | 3 | AAG30425 Arabidops |
| 46 | 650 | 57.5 | 141 | 3 | AAG37516 Arabidops |
| 47 | 646.5 | 57.2 | 121 | 3 | AAG31659 Arabidops |
| 48 | 646 | 57.1 | 142 | 3 | AAG31749 Arabidops |
| 49 | 641 | 56.7 | 142 | 3 | AAG40309 Arabidops |
| 50 | 640 | 56.6 | 143 | 3 | AAG44462 Arabidops |
| 51 | 640 | 56.6 | 143 | 3 | AAG47168 Arabidops |
| 52 | 606 | 53.6 | 133 | 3 | AAG47168 Arabidops |
| 53 | 603 | 53.3 | 184 | 8 | ADY58872 Plant pol |
| 54 | 557 | 49.2 | 207 | 5 | ADY11571 Plant ful |
| 55 | 488 | 44.2 | 102 | 3 | AAG37517 Arabidops |
| 56 | 477 | 42.2 | 134 | 8 | ADY49568 Arabidops |
| 57 | 426 | 37.7 | 137 | 8 | ADY2686 Arabidops |
| 58 | 426 | 37.7 | 137 | 8 | ADY2686 Arabidops |
| 59 | 413.5 | 36.6 | 219 | 3 | AAG05537 Arabidops |
| 60 | 411.5 | 36.4 | 159 | 3 | AAG30701 Arabidops |
| 61 | 407 | 36.0 | 221 | 3 | AAG17322 Arabidops |
| 62 | 392 | 34.7 | 240 | 8 | ADY04466 Plant ful |
| 63 | 392 | 34.7 | 240 | 8 | ADY04466 Plant ful |
| 64 | 392 | 34.7 | 245 | 8 | ADY10819 Arabidops |
| 65 | 389 | 34.4 | 245 | 8 | ADY89634 Plant ful |
| 66 | 386 | 34.1 | 131 | 3 | AAB32624 Arabidops |
| 67 | 381 | 33.7 | 96 | 3 | AAB32962 Arabidops |
| 68 | 380 | 33.6 | 220 | 4 | AAG79106 Arabidops |
| 69 | 380 | 33.6 | 220 | 5 | AAB84307 Arabidops |
| 70 | 380 | 33.6 | 220 | 7 | AAB59037 Arabidops |
| 71 | 380 | 33.6 | 220 | 7 | AAB59034 Arabidops |
| 72 | 380 | 33.6 | 220 | 7 | AAB59034 Arabidops |
| 73 | 380 | 33.6 | 220 | 9 | ADY77622 Arabidops |
| 74 | 377.5 | 33.4 | 219 | 3 | AAG30570 Arabidops |
| 75 | 375.5 | 33.2 | 235 | 8 | ADY04998 Arabidops |
| 76 | 375.5 | 33.2 | 276 | 8 | ADY07331 Plant ful |
| 77 | 363 | 32.1 | 85 | 3 | AAB32906 Arabidops |
| 78 | 349 | 30.9 | 406 | 8 | ADY2707 Plant ful |
| 79 | 347.5 | 30.7 | 144 | 3 | AAG30702 Arabidops |
| 80 | 345 | 30.5 | 74 | 3 | AAG47157 Arabidops |
| 81 | 343.5 | 30.4 | 218 | 4 | AAB58279 Arabidops |
| 82 | 340 | 30.1 | 74 | 3 | AAG20288 Arabidops |
| 83 | 336 | 29.7 | 188 | 4 | AAG79107 Arabidops |
| 84 | 334 | 29.5 | 113 | 3 | AAB32553 Arabidops |
| 85 | 328.5 | 29.0 | 134 | 3 | AAB31660 Arabidops |
| 86 | 325 | 28.7 | 177 | 3 | AAG17323 Arabidops |
| 87 | 324 | 28.6 | 75 | 3 | AAB32576 Arabidops |
| 88 | 304 | 26.9 | 68 | 3 | AAB32568 Arabidops |
| 89 | 303 | 26.8 | 77 | 3 | AAB32944 Arabidops |
| 90 | 298.5 | 26.5 | 155 | 3 | AAG17324 Arabidops |
| 91 | 298.5 | 26.4 | 79 | 3 | AAG20287 Arabidops |
| 92 | 298.5 | 26.4 | 79 | 3 | AAG47156 Arabidops |
| 93 | 295 | 26.4 | 69 | 3 | AAG20286 Arabidops |
| 94 | 295 | 26.1 | 69 | 3 | AAG40307 Arabidops |
| 95 | 295 | 26.1 | 70 | 3 | AAG27458 Arabidops |
| 96 | 294 | 26.0 | 154 | 3 | AAG05538 Arabidops |
| 97 | 290 | 25.6 | 66 | 3 | AAG47196 Arabidops |

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OM protein - protein search, using sw model

Run on: March 2, 2006, 05:11:44 ; Search time 38 Seconds
(without alignments)
557.044 Million cell updates/sec

Title: US-10-767-701-44293

Perfect score: 1131

Sequence: 1 MGQSLIYAFVARGVTILAR.....IITALLIILISVCHGPKCH 220

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | ID | Description |
|------------|-------|--------------------|--------------|---------------------|
| 1 | 1016 | 89.8 | 220 2 T00801 | probable synaptob |
| 2 | 995 | 88.0 | 221 2 F84741 | probable synaptob |
| 3 | 988.5 | 87.4 | 229 2 F86180 | hypothetical prote |
| 4 | 732.5 | 64.8 | 240 2 T47589 | synaptobrevin-like |
| 5 | 718 | 63.5 | 175 2 D86180 | hypothetical prote |
| 6 | 646.5 | 57.2 | 212 2 T04630 | probable synaptob |
| 7 | 413.5 | 36.6 | 219 2 B71423 | synaptobrevin homo |
| 8 | 411.5 | 36.4 | 159 2 C84647 | hypothetical prote |
| 9 | 377.5 | 33.4 | 219 2 JC7258 | probable synaptob |
| 10 | 377 | 33.3 | 69 2 E86180 | vesicle-associated |
| 11 | 295 | 26.1 | 60 2 D44088 | hypothetical prote |
| 12 | 274 | 24.2 | 60 2 T39073 | homeotic protein H |
| 13 | 200.5 | 17.7 | 121 2 S31250 | synaptobrevin homo |
| 14 | 185 | 16.4 | 117 2 S47654 | synaptobrevin homo |
| 15 | 185 | 16.4 | 223 2 T33239 | integral membrane |
| 16 | 175 | 15.5 | 109 2 S62059 | synaptobrevin SNB- |
| 17 | 174.5 | 15.4 | 115 2 J88504 | synaptobrevin homo |
| 18 | 174.5 | 15.4 | 719 2 B88504 | protein B0361.8 (I |
| 19 | 169.5 | 15.0 | 132 2 UC1522 | synaptobrevin isofo |
| 20 | 169.5 | 15.0 | 152 2 B38315 | synaptobrevin 1.8o |
| 21 | 167.5 | 14.8 | 116 2 JN0011 | synaptobrevin 2 - |
| 22 | 167.5 | 14.8 | 116 2 B34288 | synaptobrevin 2 - |
| 23 | 167.5 | 14.8 | 116 2 T33477 | synaptobrevin 2 - |
| 24 | 160 | 14.1 | 211 2 S52747 | synaptobrevin SEC2 |
| 25 | 153 | 13.5 | 125 2 S52747 | synaptobrevin - lo |
| 26 | 149.5 | 13.2 | 118 2 A38315 | Vamp1 protein - hu |
| 27 | 149.5 | 13.2 | 118 2 A34288 | synaptobrevin 1 - |
| 28 | 147 | 13.0 | 118 2 A32146 | vesicle-associated |
| 29 | 145.5 | 12.9 | 2 A32146 | vesicle-associated |

| | | | | |
|-----|-------|------|---------------|---------------------|
| 30 | 145.5 | 12.9 | 209 2 T40099 | probable synaptob |
| 31 | 145.5 | 12.9 | 251 2 S64927 | probable membrane |
| 32 | 143.5 | 12.7 | 103 2 S35077 | cellubrevin - rat |
| 33 | 142 | 12.6 | 260 2 T09023 | hypothetical prote |
| 34 | 138.5 | 12.2 | 508 2 F86458 | unknown protein, 7 |
| 35 | 136.5 | 12.1 | 198 2 TR0228 | unknown protein, 7 |
| 36 | 128 | 11.3 | 254 2 T04067 | Xenopus 1 protein - |
| 37 | 128 | 11.3 | 263 2 C86253 | hypothetical prote |
| 38 | 120 | 10.6 | 145 2 T21318 | hypothetical prote |
| 39 | 118.5 | 10.5 | 197 2 T39412 | hypothetical prote |
| 40 | 115.5 | 10.2 | 110 2 S35107 | hypothetical prote |
| 41 | 114 | 10.1 | 200 2 T52162 | probable snare pro |
| 42 | 111 | 9.8 | 200 2 S38053 | cell division cont |
| 43 | 97 | 8.6 | 257 2 A89456 | protein F5544.1 (I |
| 44 | 95 | 8.4 | 102 2 S44781 | G30A5.4 protein - |
| 45 | 94.5 | 8.4 | 102 2 T24909 | hypothetical prote |
| 46 | 91 | 8.0 | 317 2 JC2110 | tropomyosin-relate |
| 47 | 91 | 8.0 | 317 2 A39793 | t-complex-type mol |
| 48 | 90 | 8.0 | 2364 1 A44159 | spectrin beta-g ch |
| 49 | 89.5 | 7.9 | 598 2 D70360 | heat shock protein |
| 50 | 89 | 7.9 | 336 2 H89988 | conserved hypochet |
| 51 | 89 | 7.9 | 647 2 T08913 | hypothetical prote |
| 52 | 89 | 7.9 | 946 2 E70001 | cell division prot |
| 53 | 88 | 7.8 | 246 2 T16252 | hypothetical prote |
| 54 | 87 | 7.7 | 299 2 T46977 | cell division cont |
| 55 | 87 | 7.7 | 554 2 A40096 | platelet-endotheli |
| 56 | 87 | 7.7 | 738 2 B84800 | probable alpha-car |
| 57 | 87 | 7.7 | 2166 2 G70163 | hypothetical prote |
| 58 | 87 | 7.7 | 77 2 D64701 | thiosome and fura |
| 59 | 86.5 | 7.6 | 161 2 A36554 | synaptobrevin SEC2 |
| 60 | 86 | 7.6 | 196 2 S51405 | hypothetical prote |
| 61 | 85.5 | 7.6 | 214 2 T47779 | conserved hypochet |
| 62 | 85.5 | 7.6 | 463 2 A81621 | Ct620 hypothetical |
| 63 | 85.5 | 7.6 | 812 2 F72044 | hypothetical prote |
| 64 | 85.5 | 7.6 | 831 2 C86581 | probable thiosome |
| 65 | 85.5 | 7.6 | 287 2 T25849 | sensory transduct |
| 66 | 85 | 7.5 | 461 2 S71628 | probable syntaxin |
| 67 | 85 | 7.5 | 284 2 T41624 | syntaxin 2 - rat |
| 68 | 84.5 | 7.4 | 284 2 A97932 | initiation factor |
| 69 | 84 | 7.4 | 290 2 C48213 | DNA-binding protei |
| 70 | 84 | 7.4 | 930 2 G95064 | hypothetical prote |
| 71 | 84 | 7.4 | 958 2 S01789 | formate acetyltran |
| 72 | 84 | 7.4 | 132 2 A63192 | pyruvate formate 1 |
| 73 | 83.5 | 7.4 | 205 2 S01789 | hypothetical prote |
| 74 | 83.5 | 7.4 | 246 2 G85615 | ribosomal protein |
| 75 | 83.5 | 7.4 | 246 2 A99752 | hypothetical prote |
| 76 | 83.5 | 7.4 | 246 2 T32000 | ABC transporter, A |
| 77 | 83.5 | 7.4 | 246 2 RSRT19 | similar to chlorom |
| 78 | 83.5 | 7.4 | 196 2 S54308 | heat shock protein |
| 79 | 83 | 7.3 | 196 2 H83879 | DNA binding protei |
| 80 | 83 | 7.3 | 196 2 S51623 | 3-oxoacyl-(acyl)-c |
| 81 | 83 | 7.3 | 1172 2 S61664 | cut14 protein - fi |
| 82 | 82.5 | 7.3 | 283 2 S64918 | vacuolar protein V |
| 83 | 82.5 | 7.3 | 1418 2 J60271 | hypothetical prote |
| 84 | 82.5 | 7.3 | 2388 2 I52300 | beta spectrin, bet |
| 85 | 82.5 | 7.3 | 3225 2 A56539 | giantin - human |
| 86 | 82.5 | 7.3 | 3259 2 H81345 | giantin - human |
| 87 | 82.5 | 7.3 | 308 2 UC7765 | hypothetical prote |
| 88 | 82.5 | 7.3 | 1120 2 E75116 | mitotic spindle as |
| 89 | 82 | 7.2 | 1792 2 K1BYT8 | myosin V - fruit f |
| 90 | 82 | 7.2 | 216 2 H82054 | dTMP kinase (EC 2. |
| 91 | 82 | 7.2 | 454 2 A64515 | 4-aminobutyrate am |
| 92 | 82 | 7.2 | 470 2 A72428 | conserved hypochet |
| 93 | 81.5 | 7.2 | 558 2 A72428 | type I restriction |
| 94 | 81.5 | 7.2 | 656 2 A38903 | type I restriction |
| 95 | 81.5 | 7.2 | 891 2 B75221 | type I restriction |
| 96 | 81 | 7.2 | 1104 2 | |
| 97 | 81 | 7.2 | | |
| 98 | 81 | 7.2 | | |
| 99 | 81 | 7.2 | | |
| 100 | 81 | 7.2 | | |
| 101 | 81 | 7.2 | | |
| 102 | 81 | 7.2 | | |

probable synaptob
probable membrane
cellubrevin - rat
hypothetical prote
unknown protein, 7
Xenopus 1 protein -
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
probable snare pro
cell division cont
protein F5544.1 (I
G30A5.4 protein -
hypothetical prote
tropomyosin-relate
t-complex-type mol
spectrin beta-g ch
heat shock protein
conserved hypochet
hypothetical prote
cell division prot
hypothetical prote
cell division cont
platelet-endotheli
probable alpha-car
hypothetical prote
thiosome and fura
synaptobrevin SEC2
hypothetical prote
conserved hypochet
Ct620 hypothetical
hypothetical prote
probable thiosome
sensory transduct
probable syntaxin
syntaxin 2 - rat
initiation factor
DNA-binding protei
hypothetical prote
formate acetyltran
pyruvate formate 1
hypothetical prote
ribosomal protein
hypothetical prote
ABC transporter, A
similar to chlorom
heat shock protein
DNA binding protei
3-oxoacyl-(acyl)-c
cut14 protein - fi
vacuolar protein V
hypothetical prote
beta spectrin, bet
giantin - human
giantin - human
hypothetical prote
mitotic spindle as
myosin V - fruit f
dTMP kinase (EC 2.
4-aminobutyrate am
conserved hypochet
type I restriction
type I restriction
type I restriction
type I restriction

Sequence Alignment between
SEQ ID NO: 44293 and SEQ ID NO: 193538

RESULT 2

US-10-219-999-41251
Sequence 41251, Application US/10219999
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Edgeton, Michael D
APPLICANT: Hinkle, Gregory J.
APPLICANT: Kovalic, David K.
APPLICANT: Liu, Jingsong
APPLICANT: Stein, Joshua
TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-10(52726)C
CURRENT APPLICATION NUMBER: US/10/219,999
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: US 60/324,109
PRIOR FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: US 60/312,544
PRIOR FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 63520
SEQ ID NO 41251
LENGTH: 220
TYPE: PRT
ORGANISM: Zea mays
US-10-219-999-41251

Query Match 100.0%; Score 1131; DB 32; Length 220;
Best Local Similarity 100.0%; Pred. No. 3.9e-100;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGOOSLIYAFVARGVILAEYTEFTGNFTTASOCIMKLPASNNKFTYNCDDHTFNVLVE 60
DB 1 MGOOSLIYAFVARGVILAEYTEFTGNFTTASOCIMKLPASNNKFTYNCDDHTFNVLVE 60
QY 61 DFTTCVAVESVGOQIPAFMDRVKEDFTYKGGKATAANSLNREFGSKLKEHMOY 120
DB 61 DFTTCVAVESVGOQIPAFMDRVKEDFTYKGGKATAANSLNREFGSKLKEHMOY 120
QY 121 CVDHPEEYSKLAKVAQVSEVKGVMENIEKVLDRGEKIELVDKTEMLRSQADPFOOG 180
DB 121 CVDHPEEYSKLAKVAQVSEVKGVMENIEKVLDRGEKIELVDKTEMLRSQADPFOOG 180
QY 181 TNVRKRWMLQNMKIKLIVLGIILIIILISVCHGFKCH 220
DB 181 TNVRKRWMLQNMKIKLIVLGIILIIILISVCHGFKCH 220

RESULT 3

US-10-219-999-54339
Sequence 54339, Application US/10219999
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Edgeton, Michael D
APPLICANT: Hinkle, Gregory J.
APPLICANT: Kovalic, David K.
APPLICANT: Liu, Jingsong
APPLICANT: Stein, Joshua
TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-10(52726)C
CURRENT APPLICATION NUMBER: US/10/219,999
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: US 60/324,109
PRIOR FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: US 60/312,544
PRIOR FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 63520
SEQ ID NO 54339
LENGTH: 220
TYPE: PRT
ORGANISM: Zea mays
US-10-219-999-54339

Query Match 100.0%; Score 1131; DB 32; Length 220;
Best Local Similarity 100.0%; Pred. No. 3.9e-100;

Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGOOSLIYAFVARGVILAEYTEFTGNFTTASOCIMKLPASNNKFTYNCDDHTFNVLVE 60
DB 1 MGOOSLIYAFVARGVILAEYTEFTGNFTTASOCIMKLPASNNKFTYNCDDHTFNVLVE 60
QY 61 DFTTCVAVESVGOQIPAFMDRVKEDFTYKGGKATAANSLNREFGSKLKEHMOY 120
DB 61 DFTTCVAVESVGOQIPAFMDRVKEDFTYKGGKATAANSLNREFGSKLKEHMOY 120
QY 121 CVDHPEEYSKLAKVAQVSEVKGVMENIEKVLDRGEKIELVDKTEMLRSQADPFOOG 180
DB 121 CVDHPEEYSKLAKVAQVSEVKGVMENIEKVLDRGEKIELVDKTEMLRSQADPFOOG 180
QY 181 TNVRKRWMLQNMKIKLIVLGIILIIILISVCHGFKCH 220
DB 181 TNVRKRWMLQNMKIKLIVLGIILIIILISVCHGFKCH 220

RESULT 4

US-10-425-115-193538
Sequence 193538, Application US/10425115
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 193538
LENGTH: 220
TYPE: PRT
ORGANISM: Zea mays
US-10-425-115-193538

Query Match 100.0%; Score 1131; DB 34; Length 220;
Best Local Similarity 100.0%; Pred. No. 3.9e-100;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGOOSLIYAFVARGVILAEYTEFTGNFTTASOCIMKLPASNNKFTYNCDDHTFNVLVE 60
DB 1 MGOOSLIYAFVARGVILAEYTEFTGNFTTASOCIMKLPASNNKFTYNCDDHTFNVLVE 60
QY 61 DFTTCVAVESVGOQIPAFMDRVKEDFTYKGGKATAANSLNREFGSKLKEHMOY 120
DB 61 DFTTCVAVESVGOQIPAFMDRVKEDFTYKGGKATAANSLNREFGSKLKEHMOY 120
QY 121 CVDHPEEYSKLAKVAQVSEVKGVMENIEKVLDRGEKIELVDKTEMLRSQADPFOOG 180
DB 121 CVDHPEEYSKLAKVAQVSEVKGVMENIEKVLDRGEKIELVDKTEMLRSQADPFOOG 180
QY 181 TNVRKRWMLQNMKIKLIVLGIILIIILISVCHGFKCH 220
DB 181 TNVRKRWMLQNMKIKLIVLGIILIIILISVCHGFKCH 220

RESULT 5

US-10-767-701-44293
Sequence 44293, Application US/10767701
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701